Microbial Community Structure under Various Wheat-Based Cropping Systems

C. Hamel[1,2], K. Hanson[1], C.A. Campbell[1,3], F. Selles[1], R. Lemke[1], B.G. McConkey[1] and R.P. Zentner[1]

[1]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, P.O.Box 1030 Airport Road, Swift Current, SK, S9H 1X3
[2]Soil Science Department, University of Saskatchewan, 51 Campus Dr. Saskatoon SK S7N 5A8
[3]ECORC, Agriculture and Agri-Food Canada, K.W. Neatby Building, Floor 4, Room 4107, 960 Carling, Ottawa ON K1A 0C6

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Abstract

The effects of cropping systems on soil biological quality are slow to develop. We sampled the soil of a 36-year old long-term experiment established on an Orthic Brown Chernozem, at Swift Current SK, in the fall of 2003, to define the long-term impact of 10 cropping systems on soil biological quality. Numerous variables related to soil function -soil pH, organic C (SOC), moisture, enzymatic activities, available N, P, and S - and soil community structure - phospholipid fatty acids (PLFA) indicators of fungal saprobes, arbuscular mycorrhizal fungi and bacterial groups - were used to describe soil quality. Soils under different cropping systems had become distinct, as revealed by discriminant analyses. Variations in SOC, and pH were most influencial in discriminating the soils. SOC varied from 2.38% under continuous wheat to 1.81% under a fallow-wheat rotation. pH went from 6.55 under fallow-wheat-wheat receiving no P-fertilizer, to 4.89, under chemical fallow – fall rye – wheat. Absence of fallow under normal fertilization increased SOC and decreased soil pH. Variations in SOC and pH were concurrent with variations in microbial community structure. Enhanced AM fungi abundance under low soil P, could compensate for the large soil P depletion created by 36 years without P fertilizer, in a fallow-wheat-wheat rotation, and P-fertilized and non-P-fertilized plots produced similar yields. The season of 2003 was dryer than normal and it remains to be seen if AM fungi can compensate for low soil available P when soil moisture is abundant.

Introduction

Microorganisms are involved in numerous soil processes related to fertility and soil physical quality. In addition to being a pool of nutrients in soil, most fungi and bacteria mineralize organic matter, making the nutrients held in organic forms available to plants. Arbuscular mycorrhizal (AM) fungi form a special group of fungi; they do not mineralize soil organic matter, for all practical purposes. They are are known as plant symbionts which physically increase the absorptive surface of root systems (Fig. 1) and in this way, help their host plants take up phosphorus, other nutrients and water. AM fungi account for approximately 25% of total soil microbial biomass in agricultural fields [10,11].

Sustainable cropping systems should maintain or improve soil biological quality. Because the impact of cropping systems on soils is often slow to develop, their influence is inferred based on general knowledge. An on-going 36-year old long-term experiment conducted in Southwest Saskatchewan was an opportunity to define the long-term impacts of cropping systems on soil fertility and microbiology.

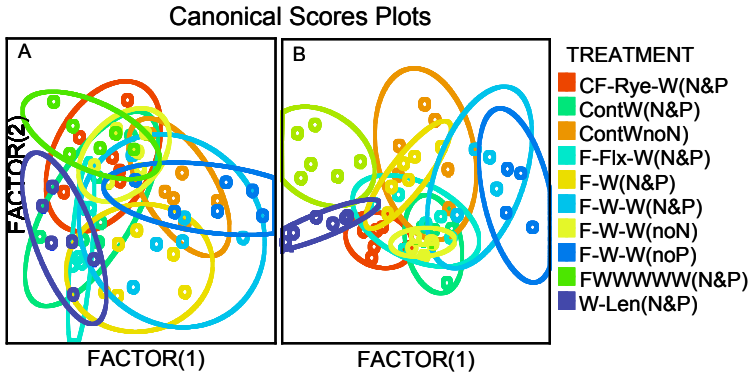
Methods

Ten different cropping systems (Table 1) were applied continuously on 0.04-ha experimental plots set up in 1967, on a Swinton silt loam (Orthic Brown Chernozem), at Swift Current SK, Canada. Crops were fertilized according to soil test, except for the treatments involving the absence of N- or P-fertilizers. The soil was conventionally tilled at a depth of 7.5 cm, each year. On September 12, 2003, the soil was sampled (0-7.5cm and 7.5cm-15cm depth). The soil variables listed in Table 2 were determined. PLFA make up cell membranes and, as such, are correlated with biomass. The PLFA C16:1_5 was used as an indicator of AM fungal biomass, and C18:2, as an indicator of the biomass of fungal decomposers. The Supelco® BAME standards were used as indicators of various soil bacterial groups' biomasses. Shannon-Weaver Biodiversity Index was calculated as - $\sum pi \ln pi$, were pi = peak area of the ith peak over the area of all peaks. The PLFA considered are listed in Table 3.

Table 1. Cropping systems included in the 36-year experiment studied

Abbreviation	Repeated crop sequence	Fertilization
CF-rye-W(N&P)*	Chemical fallow, Fall rye, Wheat	As recommended
ContW(N&P)	Continuous wheat	As recommended
ContW(noN)	Continuous wheat	No N
F-flax-W(N&P)	Fallow, Flax, Wheat	As recommended
F-W(N&P)	Fallow, Wheat	As recommended
F-W-W(N&P)	Fallow, Wheat, Wheat	As recommended
F-W-W(noP)	Fallow, Wheat, Wheat	No P
F-W-W(noN)	Fallow, Wheat, Wheat	No N
F-W-W-W-W-W(N&P)	Fallow followed by 5 yrs of Wheat	As recommended
W-len(N&P)	Wheat, Lentil	As recommended

* Samples were taken from the crop rotation phase underlined



Discriminant variables: C14:0 and isoC15, fungal saprobes, AM fungi, C15:0, C:16:0, C17:0

Discriminant variables: pH, organic C, mineralizable C, soil microbial biomass C and N, dehydrogenase, phosphatase and arylsulfatase activities, extractible PO_4, NO_3 and NH_4, but not soil moisture.

Figure 2. Crop rotations influenced soil fertility and microbiology as revealed by (A) microbial phospholipid fatty acids (PLFA) extracted from soil (*Wilks' lambda* < 0.00005; *n*=60) and (B) soil biology and fertility - related variables (*Wilks' lambda* < 0.00005; *n*=60) discrimination of the soils under different rotations. Variables with red underline, were driving the systems.

Table 2. Variables

- Soil pH
- Soil organic C [1]
- Mineralizable C [2]
- Dehydrogenase activity [3]
- ß-glucosidase activity [4]
- Phosphatase activity [5]
- Soil extractable PO_4 [6]
- Soil extractable NO_3 [7]
- Soil extractable NH_4 [8]
- Soil available SO_4 [9]
- Soil phospholipid fatty acids [10]
- Shannon-Weaver biodiversity index
- Soil microbial biomass C [11]
- Soil microbial biomass N [11]
- Grain yield

Soil variables were analyzed using 2-way randomized block design (cropping systems x depth, in 3 blocks) design, while PO_4 and grain yield was analysed using 1-way randomized block, as soil depth was not involved in these cases. Interactions were absent; main effects of cropping systems are presented. Anova were conducted with CoStat 6.003, and discriminant analyses, using Systat 10.

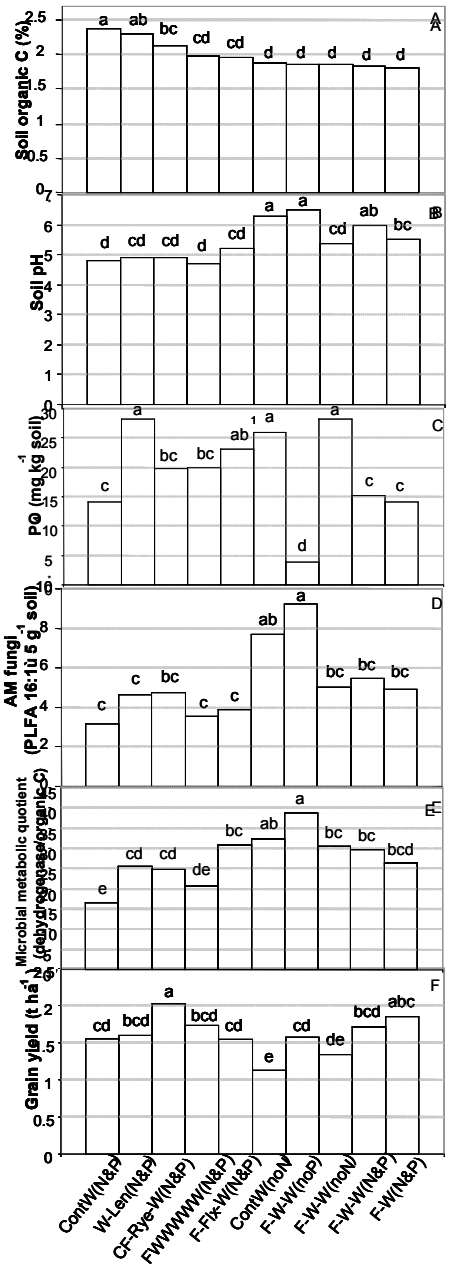


Figure 3. Impact of cropping systems on (A) soil organic C, (B) soil pH, (C) soil available P,(D) AM fungi abundance, (E) microbial efficiency, and (F) grain yield. Bars associated with the same letter are not different at the P= 0.05 level, according to a protected LSD test. n= 6 except for grain yield and PO_4, where n= 3.

Table 3. Correlation coefficients obtained from backward stepwise regression analyses, which were conducted to define the relationships between PLFA indicators of AM fungi, fungal decomposers and bacterial groups, and soil pH or organic C. +, *, **, ***, ****, indicate significance at the 0.1, 0.05, 0.01, 0.005 and <0.005 levels; n= 60.

PLFA	Soil pH		Organic C	
	P<0.0005 R^2=0.88		P<0.0005 R^2=0.67	
	Regression coefficient	P value	Regression coefficient	P value
Biodiversity			-1.4	*
AM fungi	0.1	*		
Fungal saprobes	-6.7	****	-0.6	+
C12:0				
C13:0	-3.0	+		
2OHC12				
3OHC12	0.3	*		
C14:0	0.1	*		
IsoC15	-0.2	***		
anteC15			-0.1	+
C15:0	-0.2	****	2.4	****
2OHC14	0.7	****		
IsoC16				
C16:0			-0.9	****
IsoC17				
C17:0	1.6	****		
2OHC16			0.1	*
C18:1c			-0.7	***
C18:1t				

Results and discussion

After 36 years, cropping systems had a profound effect on soil microbial community structure (Fig.2 A) and on soil fertility (Fig. 2B). All the soil variables measured, except soil moisture, significantly contributed to differentiate soils under different cropping system, according to the stepwise discriminant analysis reported in Fig. 2B. Soil pH and organic C level were the variables driving the system, as revealed by their large and inverse weight in discriminant functions 1 and 2 of the analysis. Soil organic C increased linearly with decreasing soil pH (P= 0.006; regression not shown, but see Fig. 3A and B). Several important components of the

soil microbial community were correlated with these two variables (Table 3). AM fungal biomass was not correlated with soil organic C, presumably because these fungi do not use organic matter as a source of C, in contrast to most other soil organisms. But the abundance of the AM fungal PLFA indicator was correlated with soil pH, decreasing rapidly and linearly from pH 6.5 to 4.5. The AM fungi marker C16:1_5 is also found in some gram negative bacteria [11]. Hydroxy fatty acids, which are common in gram negative bacteria [12], were either unaffected by pH or less abundant at low pH, just like the AM fungal indicator (Table 3). This suggests that the impact of pH on AM fungi may in fact be less prononced than it may seem from Fig. 4. We need to examine the effect of pH on C16:1_5 in the neutral fatty acid (NLFA) fraction of soil extracted lipid, as the AM fungal indicator in the NLFA fraction is more specific [13].

After 36 years with no P fertilization, plots in F-W-W(noP) were depleted in soil available P (Fig. 3C). Wheat yield in these plots, however, was not lower than in the F-W-W(N&P), which was fertilized as recommended (Fig. 3F). The AM fungal PLFA indicator was more abundant in the F-W-W(no-P) plots (Fig. 3D) and, presumably, AM fungi compensated for reduced P availability by effectively improving root system P extraction ability. The summer of 2003 was dry, and drought may have limited the yield potential in the fertilized plots. If the year had been less dry, the fertilized F-W-W(N&P) plots might have produced a higher yield than the F-W-W(noP) plots, unlike what we observed. It is also possible that the beneficial effect of AM fungi on yield is stronger in a dry year, as these fungi are known to reduce drought stress in crop plants [14], in addition to improving P uptake.

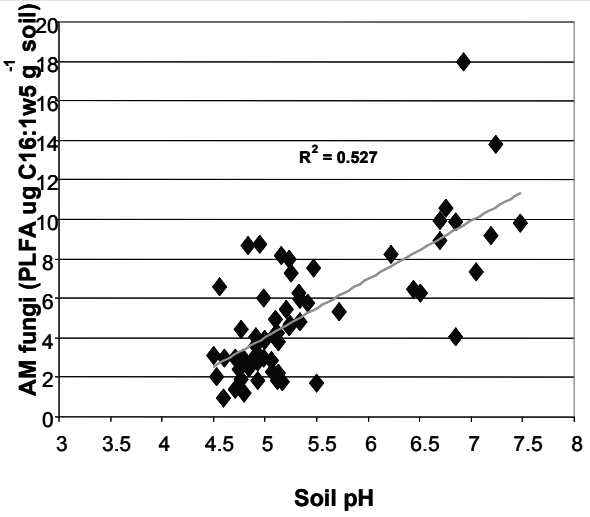


Figure 4. Relationship between soil pH and the PLFA indicator of AM fungi, as reavealed by regression analysis (*P* values for the regression and the coefficient of x are <0.00005; n=60).

Soil with inadequate fertilization had the highest microbial metabolic quotient (dehydrogenase activity/soil organic C) (Fig.3E). This may indicate an increased performance of microbial metabolism or communities under suboptimal conditions. But, it may also, and more likely reflect the fact that AM fungi, which are more abundant under limited fertility conditions, tap directly on the plants – an extraneous C source – to fullfil their C needs, giving a semblance of improved overall microbial efficiency. The latter hypothesis is supported by a positive correlation between the abundance of the AM fungi PLFA indicator and microbial metabolic quotient, that was calculated with the data from all cropping systems.

The unexpectedly good grain yield obtained in F-W(N&P), as compared to other cropping systems, is probably due to a previous year in fallow for this cropping system, in contrast to all others which were in production in 2002 (Table 1). F-W(N&P) plots may have had more water than those of other cropping systems, and water was limiting in 2003. The highest grain yield in CF-Rye-W(N&P) was explained by superior water stable soil aggregation, elsewhere[15].

Conclusions

- Absence of fallow under normal fertilization increased soil organic C and decreased pH.
- Variations in soil organic C and pH with cropping systems had the largest influences on the soil systems and on their biological quality.
- Soil organic C- and pH-related modifications were concurrent with changes in microbial community structure.
- Abundance of AM fungi was correlated with soil pH, decreasing rapidly from pH 6.5 to 4.5.
- Enhanced AM fungi abundance can compensate for the soil P depletion created by 36 years with no P fertilization, in F-W-W.

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